Supplemental Fig. 5. **Distribution of pI values for DEFLs in *Arabidopsis thaliana*.**

The percentage of genes having a predicted isoelectric point (pI) of x ± 0.25 pH units is

plotted for all predicted mature peptides. Signal peptide cleavage sites were predicted by

the SignalP server (http://www.cbs.dtu.dk/services/SignalP/). In cases where the neural

network and HMM results were in disagreement, or where multiple putative cleavage

sites had high probability, the consensus of other subgroup members was used to identify

the best cleavage site prediction. pI values for the mature peptide portion only were

determined using the ExPASy compute pI/Mw tool

(http://us.expasy.org/tools/pi_tool.html).